Search Paper 15

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  *    >>>>>>>>>>>>> NEW SUNDAY HOURS ]]] <<<<<<<<<<<<<                *
  *                                                                  *
  *    The APS is available:                                         *
  *            6:30am - 9:00pm Monday through Friday                 *
  *            7:30am - 5:00pm Saturday, Sunday, Holidays            *
  *                                                                  *
  *      APS is unavailable Thanksgiving Day, Christmas Day,         *
  *      and New Year's Day.                                         *
  *                                                                  *
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FILE 'USPAT' ENTERED AT 16:07:49 ON 27 SEP 1997

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  *              W E L C O M E   T O   T H E                       *
  *         U. S.   P A T E N T   T E X T   F I L E                *
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=> s library (p)((different or more than one or multiple) (3a) species)
         13174 LIBRARY
          4827 LIBRARIES
         14554 LIBRARY
                 (LIBRARY OR LIBRARIES)
       1112815 DIFFERENT
            88 DIFFERENTS
       1112821 DIFFERENT
                 (DIFFERENT OR DIFFERENTS)
       1829146 MORE
            97 MORES
       1829151 MORE
                 (MORE OR MORES)
       1994923 ONE
        185835 ONES
       1996472 ONE
                 (ONE OR ONES)
        151387 MORE THAN ONE
                 (MORE(1W)ONE)
        332588 MULTIPLE
         17355 MULTIPLES
        340045 MULTIPLE
                 (MULTIPLE OR MULTIPLES)
         96481 SPECIES
L1           91 LIBRARY (P)((DIFFERENT OR MORE THAN ONE OR MULTIPLE) (3A) S
PEC
                 IES)

=> s l1 (p) (pool? or same)
         41899 POOL?
       1630426 SAME
           137 SAMES
       1630434 SAME
                 (SAME OR SAMES)
L2           36 L1 (P) (POOL? OR SAME)

=> d l1 1-10 kwic

US PAT NO:      5,670,319 :IMAGE AVAILABLE:              L1: 1 of 91

DETDESC:

DETD(54)

 Libraries, either cDNA or genomic, are screened with probes designed
to identify the gene of interest or the protein encoded by it. For cDNA
expression libraries, suitable probes include monoclonal and
polyclonal antibodies that recognize and specifically bind to a TRAF
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polypeptide. For cDNA **libraries**, suitable probes include carefully selected oligonucleotide probes (usually of about 20-80 bases in length) that encode known or suspected portions of a TRAF polypeptide from the same or **different species**, and/or complementary or homologous cDNAs or fragments thereof that encode the same or a similar gene. Appropriate probes for screening genomic DNA **libraries** include, without limitation, oligonucleotides, cDNAs, or fragments thereof that encode the same or a similar gene, and/or homologous genomic DNAs or fragments thereof. Screening the cDNA or genomic **library** with the selected probe may be conducted using standard procedures as described in Chapters 10-12 of Sambrook et al., Molecular. . .

US PAT NO: 5,667,780 :IMAGE AVAILABLE: L1: 2 of 91

DRAWING DESC:

DRWD(49)

Libraries are screened with probes designed to identify the gene of interest or the protein encoded by it. For cDNA expression **libraries**, suitable probes include, e.g., monoclonal or polyclonal antibodies that recognize and specifically bind to the SMDF; oligonucleotides of about 20-80 bases in length that encode known or suspected portions of the SMDF cDNA from the same or **different species**; and/or complementary or homologous cDNAs or fragments thereof that encode the same or a similar gene. Appropriate probes for screening genomic DNA **libraries** include, but are not limited to, oligonucleotides, cDNAs, or fragments thereof that encode the same or a similar gene, and/or homologous genomic DNAs or fragments thereof. Screening the cDNA or genomic **library** with the selected probe may be conducted using standard procedures as described in chapters 10-12 of Sambrook et al., Molecular. . .

US PAT NO: 5,665,862 :IMAGE AVAILABLE: L1: 3 of 91

DETDESC:

DETD(58)

As . . . when aligned. For instance, FIG. 3 includes the alignment of several EGF-like domains of various cloned forms of ARIA from **different species**. The sequences are aligned by the conserved cysteine residues present in each variant. Analysis of the alignment of only the EGF-like domains of the ARIA clones shown in FIG. 3 can give rise to the generation of a degenerate **library** of polypeptides comprising potential EGF-like sequences represented by the general formula (SEQ ID NO:46):

US PAT NO: 5,662,898 :IMAGE AVAILABLE: L1: 4 of 91

DETDESC:

DETD(49)

Genes . . . maintains the APS-conferring ability further characterized. Whereas the host organism lacking the ability to produce the APS may be a **different species** to the organism from which the APS derives, a variation of this technique involves the transformation of host DNA into. . . of their sequence homology to the biosynthetic genes of the known compounds. Techniques suitable for cloning by homology include standard **library** screening by DNA hybridization.

US PAT NO: 5,658,789 :IMAGE AVAILABLE: L1: 5 of 91

DETDESC:

DETD(16)

Accordingly, oligonucleotide probes complementary to portions of these sequences may be used to probe any desired cDNA **library** using standard molecular biology techniques to identify related sequences from other cells and tissues within the same species or to identify related sequences from **different species**.

US PAT NO: 5,658,727 :IMAGE AVAILABLE: L1: 6 of 91

DETDESC:

DETD(242)

The size of the **library** can vary depending on a number of factors, particularly the method in which the **library** is produced. As used herein, size connotes the complexity or diversity of the **library**, that is the number of **different species** making up the **library**, rather than the absolute number of particles in the **library**.

DETDESC:

DETD(243)

Thus, where a **library** is produced by first separately cloning two repertoires of genes, corresponding to the first and second polypeptides, the resulting **library** size after randomly combining the two repertoires in the form of a dicistronic vector is greatly increased. For example, consider. . . chain and heavy chain variable antibody gene repertoires, each having 10.sup.6 different members. Combining the two repertoires theoretically yields a **library** of 10.sup.12 possible **different** dicistronic vector **species**.

DETDESC:

DETD(247)

For . . . all 16 residue positions through all possible combinations with a choice of 20 different amino acids would theoretically produce a **library** of 20.sup.16 **different species**, or 6.times.10.sup.20 **different species**.

DETDESC:

DETD(252)

The . . . the above particle segregation methods provides a means for screening a population of filamentous phage particles present in a phage **library** of this invention. As applied to a phage **library**, screening can be utilized to enrich the **library** for one or more particles that express a heterodimer having a preselected ligand binding specificity. Where the **library** is designed to contain **multiple species** of heterodimers that all have some detectable measure of ligand binding activity, but differ in protein structure, antigenicity, ligand binding affinity or avidity, and the like, the screening methods can be utilized sequentially to first produce a **library** enriched for a preselected binding specificity, and then to produce a second **library** further enriched by further screening comprising one or more isolated phage particles. Methods for measuring ligand binding activities, antigenicity and. . .

CLAIMS:

CLMS(27)

27. The **library** of cl[redacted] 26 wherein said **library** conta[redacted] at least 10.sup.7 **different species** of said vector.

US PAT NO: 5,656,593 :IMAGE AVAILABLE: L1: 7 of 91

SUMMARY:

BSUM(35)

Thus, in view of this disclosure, skilled genetic engineers can isolate genes from cDNA or genomic **libraries** of various **different species** which encode appropriate amino acid sequences, or construct DNAs from oligonucleotides, and then can express them in various types of. . .

US PAT NO: 5,652,343 :IMAGE AVAILABLE: L1: 8 of 91

DETDESC:

DETD(61)

Libraries are screened with probes designed to identify the gene of interest or the protein encoded by it. For cDNA expression **libraries**, suitable probes usually include mono- and polyclonal antibodies that recognize and specifically bind to the desired protein; oligonucleotides of about 20-80 bases in length that encode known or suspected portions of the selectin ligand cDNA from the same or **different species**; and/or complementary or homologous cDNAs or their fragments that encode the same or similar gene.

US PAT NO: 5,652,132 :IMAGE AVAILABLE: L1: 9 of 91

DETDESC:

DETD(70)

The . . . recognized that residues 31-34 form a putative consensus sequence (SEQ ID NO: 5) Cys-Gly-Pro-Cys, typically involved in redox reactions. A **library** search and comparison performed with LMW sequence 2-38 confirmed this notion by revealing similarity of this sequence to thioredoxin of **different species** (for instance 60% similarity in a 38 amino acid overlap with thioredoxin of E. coli).

US PAT NO: 5,650,489 :IMAGE AVAILABLE: L1: 10 of 91

DETDESC:

DETD(176)

It is further envisioned that a limited **library** of the invention may be useful as a vaccine for a pathogen that presents with a diversity of epitopes. For. . . By altering the VSG epitope, trypanosome evades immune recognition. Similarly, malarial parasites are found to express diverse antigenic epitopes across **species**, at **different** stages of the life cycle, and within subspecies. Thus a peptide **library** of restricted diversity could immunize against the variable antigenic diversity presented by trypanosome or malarial parasites. A limited **library** may have application as a vaccine in any case where immunity to a range of antigens is desired.

DETDESC:

DETD(205)

Both patterns exhibit 21 distinct peaks, indicating the presence of at least 21 **different** peptide **species** within each **library**. The SPPS pattern, however, exhibits significantly greater peaks at #1, 2, 3, 4, 5, 6, and 7, indicating that the SPPS **library** contained a greater concentration of peptides 1-7 than of peptides 8-21. The increased number of peptides 1-7 demonstrates that these. . .

=> d l2 1-10 kwic

US PAT NO: 5,670,319 :IMAGE AVAILABLE: L2: 1 of 36

DETDESC:

DETD(54)

Libraries, either cDNA or genomic, are screened with probes designed to identify the gene of interest or the protein encoded by it. For cDNA expression **libraries**, suitable probes include monoclonal and polyclonal antibodies that recognize and specifically bind to a TRAF polypeptide. For cDNA **libraries**, suitable probes include carefully selected oligonucleotide probes (usually of about 20-80 bases in length) that encode known or suspected portions of a TRAF polypeptide from the **same** or **different species**, and/or complementary or homologous cDNAs or fragments thereof that encode the **same** or a similar gene. Appropriate probes for screening genomic DNA **libraries** include, without limitation, oligonucleotides, cDNAs, or fragments thereof that encode the **same** or a similar gene, and/or homologous genomic DNAs or fragments thereof. Screening the cDNA or genomic **library** with the selected probe may be conducted using standard procedures as described in Chapters 10-12 of Sambrook et al., Molecular. . .

US PAT NO: 5,667,780 :IMAGE AVAILABLE: L2: 2 of 36

DRAWING DESC:

DRWD(49)

Libraries are screened with probes designed to identify the gene of interest or the protein encoded by it. For cDNA expression **libraries**, suitable probes include, e.g., monoclonal or polyclonal antibodies that recognize and specifically bind to the SMDF; oligonucleotides of about 20-80 bases in length that encode known or suspected portions of the SMDF cDNA from the **same** or **different species**; and/or complementary or homologous cDNAs or fragments thereof that encode the **same** or a similar gene. Appropriate probes for screening genomic DNA **libraries** include, but are not limited to, oligonucleotides, cDNAs, or fragments thereof that encode the **same** or a similar gene, and/or homologous genomic DNAs or fragments thereof. Screening the cDNA or genomic **library** with the selected probe may be conducted using standard procedures as described in chapters 10-12 of Sambrook et al., Molecular. . .

US PAT NO: 5,662,898 :IMAGE AVAILABLE: L2: 3 of 36

DETDESC:

DETD(49)

Genes . . . maintains the APS-conferring ability further characterized. Whereas the host organism lacking the ability to produce the APS may be a **different species** to the organism from which the APS derives, a variation of this technique involves the transformation of host DNA into the **same** host which has had its APS-producing ability disrupted by mutagenesis. In this method, an APS-producing organism is mutated and non-APS. . . of their sequence homology to the

biosynthetic genes of the known compounds. Techniques suitable for cloning by homology include standard **library** screening by DNA hybridization.

US PAT NO: 5,658,789 :IMAGE AVAILABLE: L2: 4 of 36

DETDESC:

DETD(16)

Accordingly, oligonucleotide probes complementary to portions of these sequences may be used to probe any desired cDNA **library** using standard molecular biology techniques to identify related sequences from other cells and tissues within the **same** species or to identify related sequences from **different species**.

US PAT NO: 5,652,343 :IMAGE AVAILABLE: L2: 5 of 36

DETDESC:

DETD(61)

Libraries are screened with probes designed to identify the gene of interest or the protein encoded by it. For cDNA expression **libraries**, suitable probes usually include mono- and polyclonal antibodies that recognize and specifically bind to the desired protein; oligonucleotides of about 20-80 bases in length that encode known or suspected portions of the selectin ligand cDNA from the **same** or **different species**; and/or complementary or homologous cDNAs or their fragments that encode the **same** or similar gene.

US PAT NO: 5,645,986 :IMAGE AVAILABLE: L2: 6 of 36

DETDESC:

DETD(277)

Telomere-enriched **libraries** were constructed from genomic DNA from seven budding yeast species and strains. Telomeric clones were identified by their ability to. . . abutting vector sequences, as would be expected for cloned telomeres. The repeat-containing clone from each species hybridized back to the **same** pattern of restriction fragments observed originally with the C. albicans or the S. cerevisiae probe used for **library** screening. Most of the bands were preferentially sensitive to Ba131 nuclease (FIG. 29) indicating that the bulk of the repeat sequences are present at the ends of chromosomes. The lengths of the tracts of repeats cloned from the **different** yeast **species** were typically between 250-600 bp, although those from the two C. tropicalis strains were only 130-175 bp. That this species. . .

US PAT NO: 5,643,774 :IMAGE AVAILABLE: L2: 7 of 36

DETDESC:

DETD(50)

Genes . . . maintains the APS-conferring ability further characterized. Whereas the host organism lacking the ability to produce the APS may be a **different species** to the organism from which the APS derives, a variation of this technique involves the transformation of host DNA into the **same** host which has had its APS-producing ability disrupted by mutagenesis. In this method, an APS-producing organism is mutated and non-APS. . . of their sequence homology to the biosynthetic genes of the known compounds. Techniques suitable for cloning by homology include standard **library** screening by DNA